2-glycoprotein I); EC 3.4.21.36 (Pancreatic Elastase)

=> d his

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(FILE 'HOME' ENTERED AT 08:55:04 ON 21 JUL 2004)
                SET COST OFF
     FILE 'HCAPLUS' ENTERED AT 08:55:31 ON 21 JUL 2004
L1
               1 S (WO99-EP9440 OR EP98-122969) /AP, PRN
                E SONDERMANN P/AU
              24 S E3,E4
L2
                E SONDERMAN P/AU
                 E HUBER R/AU
           1139 S E3-E14, E40-E48
L3
                E HUEBER R/AU
               6 S E3,E4,E6
L4
                E HEUBER R/AU
                E JACOB U/AU
              50 S E3,E7
L5
                E MAX PLANCK/PA,CS
                E MAXPLANC/PA, CS
          92521 S (MAXPLANC? OR MAX()PLANC?)/PA,CS
Ь6
               3 S E45-E49
L7
                E MAX-PLA/PA,CS
                E MAXPLA/PA, CS
                E MAX PLA/PA,CS
L8
              3 S E5-E7
                E MAX PLAU/PA, CS
              10 S E5-E14
L9
                E FC RECEPTOR/CT
                E E58+ALL
L10
             19 S E2
                E FC RECEPTOR/CT
                E E31+ALL
            202 S E2 (L) (IIB OR IIC)
L11
                E FC
                E FCGAMMA
L12
              3 S E3(L) (IIB OR IIC)
              1 S E10
L13
             84 S E26-E29
L14
            529 S FC?(L)(IIB OR IIC OR RIIB OR RIIC OR R()(IIB OR IIC))
L15
            414 S FC(L) RECEPTOR? (L) (IIB OR IIC OR RIIB OR RIIC OR R() (IIB OR II
L16
L17
            358 S L16 (L) GAMMA
            398 S L15 (L) ?GAMMA?
L18
            358 S L16 (L) ?GAMMA?
L19
            452 S L17-L19,L10-L14
L20
L21
            121 S L15-L19 NOT L20
L22
             46 S L21 AND IMMUNOGLOBULIN
L23
            397 S L20 AND IMMUNOGLOBULIN
             55 S L20 NOT L23
L24
L25
            498 S L20, L22-L24
L26
             75 S L10-L24 NOT L25
             37 S L25 AND RECOMBIN?
L27
L28
             38 S L25 AND CHIMER?
             67 S L27, L28
L29
                E RECOMBINANT/CT
                E E47+ALL
          42218 S E1+NT
L30
                E E7+ALL
          16654 S E3, E4, E2+NT
L31
             26 S L25 AND L30, L31
L32
                E IMMUNOGLOGULIN/CT
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E IMMUNOGLOBULIN/CT
                E E35+ALL
L33
          72507 S E9+OLD, NT, PFT, RT
L34
             56 S L33 AND L29, L32
L35
             12 S L29, L32 NOT L34
                SEL DN AN 6
              1 S L35 AND E1-E3
L36
              8 S L34 NOT ?GAMMA?
L37
L38
              7 S L37 AND TYPE() (II OR IIB OR IIC OR IIA)
              6 S L37 AND TYPE()(IIB OR IIC)
L39
L40
              6 S L37 AND IGG()TYPE()(IIB OR IIC)
             5 S L40 NOT MHC/TI
L41
             3 S L37 NOT L41
L42
L43
            57 S L34,L36,L41
L44
            11 S L2-L9 AND L25
L45
              3 S L44 AND (RECOMB? OR CHIMER?)
L46
             3 S L1,L45
L47
              8 S L44 NOT L46
              7 S L47 NOT SHIP
L48
             10 S L46, L48
L49
L50
             19 S L43 AND (PY<=1998 OR PRY<=1998 OR AY<=1998)
             27 S L49, L50
L51
L52
             27 S L51 AND (IIB OR IIC OR ?RIIB OR ?RIIC OR FC? OR ?GAMMA? OR IM
     FILE 'HCAPLUS' ENTERED AT 09:30:47 ON 21 JUL 2004
                SEL RN L1
     FILE 'REGISTRY' ENTERED AT 09:31:09 ON 21 JUL 2004
L53
             21 S E4-E24
1.54
             12 S L53 AND PROTEIN/FS
L55
              1 S L54 AND 185/SQL
     FILE 'HCAPLUS' ENTERED AT 09:31:43 ON 21 JUL 2004
L56
              1 S L55
     FILE 'REGISTRY' ENTERED AT 09:31:55 ON 21 JUL 2004
     FILE 'HCAPLUS' ENTERED AT 09:33:19 ON 21 JUL 2004
           5300 S FC? (L) (III OR RIII OR R III)
L57
           1349 S L57(L)?GAMMA?
L58
           1054 S FC(L) RECEPTOR?(L) (III OR RIII OR R III) (L) ?GAMMA?
L59
L60
           1349 S L58, L59
           148 S L60 AND (RECOMBINA? OR CHIMER?)
L61
             18 S L60 AND L30, L31
L62
            149 S L61,L62
L63
            132 S L63 AND IMMUNOGLOBULIN
L64
            17 S L63 NOT L64
L65
L66
            103 S L64 AND (PY<=1998 OR PRY<=1998 OR AY<=1998)
            14 S L2-L9 AND L60
L67
             2 S L67 AND L63
L68
             1 S L68 NOT RECOMBINASE
L69
             12 S L67 NOT L68
L70
L71
             10 S L70 NOT (ULTRASONIC OR INTERLEUKIN)/TI
L72
             34 S L69,L71,L52
            103 S L66 AND ?GAMMA?
L73
L74
            103 S L73 AND FC?
L75
            83 S L74 AND III
L76
            94 S L74 AND ?RIII
            103 S L75, L76
L77
              9 S L74 NOT L76
L78
L79
             8 S L78 AND TYPE III
            103 S L77, L76
L80
L81
            12 S L80 AND P/DT
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SEL DN AN 1 3 4 8
             4 S E25-E36
L83
            96 S L80 NOT L52, L72, L82
               SEL DN AN 30 50 51 71 85 93
             6 S E37-E54
            44 S L52, L72, L82, L84 AND L1-L52, L56-L84
            30 S L85 AND (PY<=1998 OR PRY<=1998 OR AY<=1998)
L86
            14 S L85 NOT L86
L87
L88
            17 S L85 AND L1-L9
            17 S L87,L88
L89
            27 S L85 NOT L89
L90
    FILE 'HCAPLUS' ENTERED AT 10:06:09 ON 21 JUL 2004
    FILE 'MEDLINE' ENTERED AT 10:06:49 ON 21 JUL 2004
               E FC RECEPTOR/CT
               E E6+ALL
               E E2+ALL
           4709 S E27
L91
               E RECOMBINANT/CT
           185 S E13+NT AND L91
L92
           497 S E77+NT AND L91
L93
           497 S L92, L93
L94
           331 S L94 AND PY<=1998
L95
           86 S L95 AND (?RIIB? OR ?RIII?)
L96
            43 S L95 AND (IIB? OR III?)
L97
           106 S L96,L97
L98
           104 S L98 AND FC?
L99
           94 S L99 AND ?GAMMA?
L100
            12 S L98 NOT L100
L101
            82 S L100/HUM
L102
            12 S L100 NOT L102
L103
            20 S L91 AND (SONDERMAN? OR HUBER ? OR HEUBER ? OR HUEBER ? OR JAC
L104
            5 S L104 AND PY<=1998
L105
             8 S L104 AND ?RIIB
L106
             5 S L104 AND ?RIII
L107
L108
            11 S L106, L107
    FILE 'MEDLINE' ENTERED AT 10:15:16 ON 21 JUL 2004
            9 S L108 NOT (JACOB C? OR JACOB A?)/AU
L109
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

July 14, 2004, 06:36:34; Search time 19 Seconds (without alignments) 502:674 Million cell updates/sec

US-09-856-933-3 1006 1 MGTPAAPPKAVLKLEPQWIN......SSKRVTITVQAPSSSPWGII 185 Title: Perfect score:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Sequence:

389414 seqs, 51625971 residues Searched:

Total number of hit's satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:* Database

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/cgm2_6/ptodata/2/iaa/6G_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence.6, Appli	83	5	13	10,	14,	15,	12	3, 4	11, 7	13	81, 7	134,	13	90,	7, 7	۲,	'n	J.	ω,	é,	o,	4	4	æ	œ	Sequence 2, Appli
	ă		٠,	٠,	٠,	٠,	0,	0,	٠,	٠,	U 2	٠.	٠,	٠.	٠.					_	_							
SUMMARIES	ΙD	US-09-245-764-6	US-08-332-562A-83	US-09-245-764-5	US-08-332-562A-132	US-09-245-764-10	US-09-245-764-14	US-09-245-764-15	-60-	US-09-245-764-3	US-09-245-764-11	US-08-332-562A-136	US-08-332-562A-81	-332-		US-08-332-562A-90	US-08-667-939A-7	US-08-433-123-7	US-08-667-939A-5	US-08-433-123-5	. US-09-245-764-8	US-08-667-939A-6	US-08-433-123-6	US-08-667-939A-4	US-08-433-123-4	US-08-667-939A-8	US-08-433-123-8	US-08-667-939A-2
*	DB	4	7	4	N	4	4	4	4	4	4	~	7	7	7	7	(1	4	7	4	4	7	4	7	4	~	4	7
	Query Match Length	170	307	170	345	170	171	171	170	171	170	283	330	330	261	87	233	233	233	233	174	233	233	254	254	233	233	254
	Query Match	92.4	91.6	91.6		87.9	7.	87.2	86.9	86.8	86.4		60.7	59.3	57.4	44.8	44.5	44.5	43.6	43.6	43.5	43.5	43.5	43.1	43.1	43.1	43.1	43.0
	Score	930	921.5	921	885.5	884	883	877	874	873	698	611	611	597	577	451	447.5	447.5	438.5	438.5	438	437.5	437.5	434	434	e,	•	433
	Result No.	П	7	ĸ	4	D.	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23	24	25	26	27

Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 18, Appl	Sequence 18, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 91, Appl	Sequence 7, Appli	Sequence 14, Appl	Sequence 31, Appl	Sequence 28, Appl	Sequence 24, Appl	Sequence 20, Appl	
US-08-433-123-2	US-08-667-939A-3	US-08-433-123-3	US-08-667-939A-20	US-08-433-123-20	US-08-667-939A-18	US-08-433-123-18	US-08-667-939A-9	US-08-433-123-9	US-08-667-939A-1	US-08-433-123-1	US-08-332-562A-91	US-09-245-764-7	US-08-833-488B-14	US-08-833-488B-31	US-08-833-488B-28	US-08-833-488B-24	US-08-833-488B-20	
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254	254	254	203	203	215	215	254	254	254	254	83	261	199	173	197	229	253	,
43.0	42.9	42.9	42.5	42.5	42.5	42.5	42.5	42.5	41.9	41.9	41.0	39.2	35.0	34.9	34.9	34.9	34.9	
433	432	432	428	428	428	428	428	428	422	422	412.5	394	352	351	351	351	351	
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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APPLICANT: Garrett, Thomas P.J.
APPLICANT: Epa, Vidana
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF PC RECEPTORS
FILT REFERENCE: 4102-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 NDSGEYTCQTGQTSLSDPVHLTVLSEWLVLQTPHLEPQEGETIVLRCHSWKDKPLVKVTF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 NDSGEYTCQTGQTSLSDPVHLIVLSEMLVLQTPHLEPQEGETIVLRCHSWKDKPLVKVTF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 APPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNGNLIPTHTQPSYRFKANN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 PONGKSKKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTLYSSKPVTITVQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.4%; Score 930; DB 4; Length 170; 100.0%; Pred. No. 3e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
92.4%; Score 930; DB
Best Local Similarity 100.0%; Pred. No. 3e-
Matches 170; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/245,764 CURRENT FILING DATE: 1999-02-05
                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/099,994
EARLIER FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: 60/073,972
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
Application US/09245764
                                                                                        APPLICANT: Powell, Maree S. APPLICANT: McKenzie, Ian F.C. APPLICANT: Maxwell, Kelly F. APPLICANT: Garrett, Thomas P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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121 FONGKSKKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTLYSSKPVTITVQ 170 RESULT 2 US-08-332-562A-83 qq ઠે

; Sequence 83, Application US/08332562A; Patent No. 5985599 | | GENERAL INFORMATION: